



QY 84 DHKLEILQGLYLIYGOVAPNANNDVAPFEVRLYKKNKDMIQTLTNKSKIQNGVGYELH 143  
 Db 213 -----KGSMDSANILDEYFPFARVLKSYVVEVIAGISAV--LGGIILN 256  
 QY 144 VGDITDLIFNSHQVLKNNYGIILLANPOFIS 177  
 Db 257 VDDSV-----SGPHLSV---TFEWILLVACFPSAIA 283

RESULT 2  
 ARG2\_YEAST  
 ID ARG2\_YEAST STANDARD; PRT; 880 AA.  
 AC P05085;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ARGININE METABOLISM REGULATION PROTEIN II.  
 GN ARG2 OR ARG81 OR YML099C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;  
 OC Saccharomycetaceae; Saccharomyces.

[1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=86220196; PubMed=3709534;  
 RA Messing F., Dubois E., Descamps F.;  
 RT "Nucleotide sequence of the ARG81 regulatory gene and amino acid  
 RT sequence homologues between ARG81 PPR1 and GAL4 regulatory  
 RL Eur. J. Biochem. 157:77-81(1986).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RA Gentles S., Bowman S., Barrell B.G., Rajandream M.A.;  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THIS PROTEIN REPRESS OR INDUCES SEVERAL GENES OR  
 CC ARGININE METABOLISM.  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -!- SIMILARITY: CONTAINS A ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR  
 CC CLUSTER DOMAIN.  
 CC  
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DR EMBL; X03940; CAA27577.1; -;  
 DR EMBL; Z46660; CAA86638.1; -;  
 DR PIR; A25064; A25064.  
 DR TRANSPAC; T00044; -;  
 DR SGD; S0004565; ARG81.  
 DR INTERPRO; IPR001138; -;  
 DR PFAM; PF00172; Zn\_clus; 1.  
 DR PROSITE; PS00463; ZN2\_CY6\_FUNGAL\_1; 1.  
 DR PROSITE; PS50048; ZN2\_CY6\_FUNGAL\_2; 1.  
 KW Transcription regulation; Activator; DNA-binding; Nuclear protein;  
 KW Zinc; Metal-binding; Arginine metabolism.  
 FT DNA\_BIND 21 48  
 FT SIMILAR 587 690 ZN(2)-CYS(6), FUNGAL-TYPE.  
 FT CONFLICT 4 4 S -> F (IN REF. 1).  
 FT CONFLICT 129 129 MISSING (IN REF. 1).  
 FT CONFLICT 283 283 F -> V (IN REF. 1).  
 FT CONFLICT 345 345 D -> V (IN REF. 1).  
 FT CONFLICT 366 366 E -> Q (IN REF. 1).  
 FT CONFLICT 549 549 T -> A (IN REF. 1).  
 FT CONFLICT 597 597 T -> S (IN REF. 1).  
 FT CONFLICT 665 665 K -> N (IN REF. 1).  
 FT CONFLICT 869 869 V -> I (IN REF. 1).  
 SEQUENCE 880 AA; 100281 MW; DA033AB2B373F415 CRC64;

Query Match 8.1%; Score 77.5; DB 1; Length 880;  
 Best Local Similarity 22.7%; Pred. No. 10;  
 Matches 37; Conservative 35; Mismatches 54; Indels 37; Gaps 8;  
 QY 45 IFIFLQL---ETAKEPCMAK-----FGPLPSKQWASSEPPCVNKV----- 82  
 Db 555 IFSLKLIQDSTALDKVRAKEIVILFSEEDDNYPKPLDTSNATTSSEPRVDVYQGLFRE 614  
 QY 83 -----SDWK---LEILQGLYLIYGOVAPNAN---YNDVAPFEVRLYKKNKDMIQTLTNKSK 132  
 Db 615 ALNENDGKTHIEFVKETPNVSADSTPSSVTPPIFNIA---TESYNKASDKILVSKTD 671  
 QY 133 IQNGVGYELH-VGDYTDLIFNSEHQVLKNNYGIILLANPO 174  
 Db 672 -ENIGTDSLYGLPNSLILLFSDCVIRVIRHNEYINLTPLVPR 713

RESULT 3  
 VS09\_ROTHA  
 ID VS09\_ROTHA STANDARD; PRT; 326 AA.  
 AC P04328;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL  
 DE GLYCOPROTEIN).  
 GN S9.

OS Human rotavirus (serotype 2 / strain Hu5).  
 OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84221410; PubMed=6328448;  
 RA Dyall-Smith M.L., Holmes I.H.;  
 RT "Sequence homology between human and animal rotavirus  
 RT serotype-specific glycoproteins."  
 RL Nucleic Acids Res. 12:3573-3982(1984).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=88044489; PubMed=2823458;  
 RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
 RA Chanock R.M., Flores J.;  
 RT "Comparison of the amino acid sequences of the major neutralization  
 RT protein of four human rotavirus serotypes."  
 RL Virology 161:153-159(1987).  
 CC -!- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.  
 CC -!- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.

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DR EMBL; X00572; CAA25236.1; -;  
 DR EMBL; A01028; CAA00124.1; -;  
 DR PIR; G27620; VGXRHU.  
 DR PIR; A93520; VGXRHD.  
 DR PFAM; PF00434; VP7; 1.  
 DR INTERPRO; IPR001963; -;  
 DR Coar protein; Transmembrane; Glycoprotein.  
 FT TRANSMEM 32 48  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SEQUENCE 326 AA; 37202 MW; 2D438F6EFC86FCB0 CRC64;

Query Match 8.1%; Score 77; DB 1; Length 326;  
 Best Local Similarity 22.8%; Pred. No. 3.6;  
 Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

VS09\_ROTTH STANDARD; PRT; 326 AA.  
ID VS09\_ROTTH STANDARD; PRT; 326 AA.  
AC P11851; 1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL  
GN S9.  
OS Human rotavirus (serotype 2 / strain HN126).  
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88044489; PubMed=2823458;  
RA Green K.Y., Midhun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
Chanock R.M., Flores J.;  
KA "Comparison of the amino acid sequences of the major neutralization  
RT protein of four human rotavirus serotypes.";  
RL Virology 161:153-159(1987).  
CC -1- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.  
CC -1- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.  
DR PIR: F27620; VGXRNH.  
DR INTERPRO: IPR001963; -.  
DR PFAM: PF00434; VP7; 1.  
DR COAT protein; Transmembrane; Glycoprotein.  
KW TRANSMEM 32 48  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 326 AA; 37246 MW; 4799219E9D6A9B1 CRC64;

RESULT 4  
VS09\_ROTTH STANDARD; PRT; 326 AA.  
ID VS09\_ROTTH STANDARD; PRT; 326 AA.  
AC P11850;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL  
GN S9.  
OS Human rotavirus (serotype 2 / strain DS1).  
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88044489; PubMed=2823458;  
RA Green K.Y., Midhun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
Chanock R.M., Flores J.;  
KA "Comparison of the amino acid sequences of the major neutralization  
RT protein of four human rotavirus serotypes.";  
RL Virology 161:153-159(1987).  
CC -1- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.  
CC -1- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.  
DR PIR: E27620; VGXRS.  
DR INTERPRO: IPR001963; -.  
DR PFAM: PF00434; VP7; 1.  
DR COAT protein; Transmembrane; Glycoprotein.  
KW TRANSMEM 32 48  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 326 AA; 37216 MW; 5D338B3BE9D6A9B5 CRC64;

Query Match 8.1%; Score 77; DB 1; Length 326;  
Best Local Similarity 22.8%; Pred. No. 3.6;  
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;  
QY 26 LWLFCSIVMLFLC-----SFSWLIFLQLETAKEPCMAK-----FGPLPSKQWQ 71  
DB 10 LTILISILNLNYILKTTMTMDYIIFRELLIALISPFVRTQNYGMVLPITGSLDAVYTN 69  
QY 72 ASSEPP-----CV-----NKVSDMKLEILQNGLYLYGOVAPNA---NYNDVAPFEV 115  
DB 70 STSGEPFLTSTLCLYYPAEAKNEISDDWENTLSOLFETKGPVGSVYFKDYNDINTFSV 129  
QY 116 --RLYKNDMIOTLTNKSQIONGVGTYELHVGDTIDLFNSEHQLVKNNTYWGILLANP 173  
DB 130 NPOLYCDYVNV-----LMRYDNTSELDASELADLIINE-----W-----LCNP 167  
QY 174 QFIS 177  
DB 168 MDIS 171

RESULT 6  
TNFA\_FELCA STANDARD; PRT; 233 AA.  
ID TNFA\_FELCA STANDARD; PRT; 233 AA.  
AC P19101;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
GN TNF OR TNFA.  
OS Fells silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BLOOD;  
RX MEDLINE=91016860; PubMed=2216740;  
RA McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;  
RL "Gene sequence of feline tumor necrosis factor alpha.";  
RN Nucleic Acids Res. 18:5563-5563(1990).

Query Match 8.1%; Score 77; DB 1; Length 326;  
Best Local Similarity 22.8%; Pred. No. 3.6;  
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;  
QY 26 LWLFCSIVMLFLC-----SFSWLIFLQLETAKEPCMAK-----FGPLPSKQWQ 71  
DB 10 LTILISILNLNYILKTTMTMDYIIFRELLIALISPFVRTQNYGMVLPITGSLDAVYTN 69  
QY 72 ASSEPP-----CV-----NKVSDMKLEILQNGLYLYGOVAPNA---NYNDVAPFEV 115  
DB 70 STSGEPFLTSTLCLYYPAEAKNEISDDWENTLSOLFETKGPVGSVYFKDYNDINTFSV 129  
QY 116 --RLYKNDMIOTLTNKSQIONGVGTYELHVGDTIDLFNSEHQLVKNNTYWGILLANP 173  
DB 130 NPOLYCDYVNV-----LMRYDNTSELDASELADLIINE-----W-----LCNP 167  
QY 174 QFIS 177  
DB 168 MDIS 171

SEQUENCE FROM N.A.  
 RC TISSUE-BONE MARROW;  
 RA Daniel S.L., Brenner C.A., Legendre A.M., Solomon A., Rouse B.T.;  
 RL Submitted (xxx-1993) to the EMBL/GenBank/DBJ databases.  
 RC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
 CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
 CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
 CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CC CONDITIONS.  
 CC -!- SUBUNIT: HOMOTRIMER.  
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC -----  
 DR EMBL: X54000; CAA37948.1; -;  
 DR EMBL: M92061; AAA30818.1; -;  
 DR FIP: S11688; S11688.  
 DR HSSP: P01375; 1TNF.  
 DR INTERPRO: IPR000478; -;  
 DR INTERPRO: IPR002959; -;  
 DR PRAM: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNECROSISPT.  
 DR PRINTS: PR01235; TNFALPHA.  
 DR PROSITE: PS00251; TNF-1; 1.  
 DR PROSITE: PS00049; TNF-2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
 FT PROPEP 1 76  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT DISULFID 145 177 BY SIMILARITY.  
 FT CONFLICT 28 28 G -> R (IN REF. 2).  
 FT CONFLICT 104 104 R -> W (IN REF. 2).  
 FT CONFLICT 151 151 L -> H (IN REF. 2).  
 FT CONFLICT 155 155 A -> T (IN REF. 2).  
 FT CONFLICT 210 210 T -> A (IN REF. 2).  
 SQ SEQUENCE 233 AA; 25322 MW; 434D239567862506 CRC64;  
 -----  
 Query Match 8.0%; Score 76.5; DB 1; Length 233;  
 Best Local Similarity 20.28; Pred. No. 2.8;  
 Matches 50; Conservative 31; Mismatches 54; Indels 113; Gaps 12;  
 QY 7 ENPFLSHRTQGAQRSSWKLWFLCSIVMLFLCSFWLIF-----IFLQLETAKEPCMAK 61  
 DB 15 EALPKKAGGPGQSGR-----CLCLSLFSLVAGATTFL-----CLLH 52  
 QY 62 FG-----PLPSKWNAS---SEPPCVN----- 80  
 DB 53 FGVIQPGREELPHGLINLPQTLRSSRTPSDKPVAVHVANPEAGOLQRLSRANAL 112  
 QY 81 -----KVSMDKLEILONGLYLYIGQV-----APNANY-----NDVAPFEVRLYKNKDMIO 126  
 DB 113 LANGVELTDNQLKVPDGLVLYISVLTGCGCPSTHLLTHAISRFVSYQTKVNLISA 172  
 QY 127 LTNKSKTON-----VGGTVELHVGOTID-----LTFNSEHQVLKNN 162  
 DB 173 I--KSPQRETPPEGAQAKPWYEPYILGGVFQLEKGRDLSTEINLPAYLDFABSGQV----- 226

QY 163 TYWCIILL 170  
 DB 227 -YFGLIAL 233  
 RESULT 7  
 ID TNFA-PAPHU STANDARD; PRT: 233 AA.  
 AC 077510;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
 GN TNF OR TNFA.  
 OS Papio hamadryas ursinus (Chacma baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Papio.  
 RP 111  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE-98147379; PubMed-9488055;  
 RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;  
 RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor  
 RT alpha.";  
 RL Mol. Immunol. 34:1041-1042(1997).  
 CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES. IT IS A CYTOKINE  
 CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
 CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
 CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CC CONDITIONS.  
 CC -!- SUBUNIT: HOMOTRIMER.  
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC -----  
 DR EMBL: AF019963; AAC31675.1; -;  
 DR INTERPRO: IPR000478; -;  
 DR INTERPRO: IPR002959; -;  
 DR PFAM: PF00229; TNF; 1.  
 DR PRINTS: PR01234; TNECROSISFCT.  
 DR PRINTS: PR01235; TNFALPHA.  
 DR PROSITE: PS00251; TNF-1; 1.  
 DR PROSITE: PS00049; TNF-2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
 FT PROPEP 1 76  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT DISULFID 145 177 BY SIMILARITY.  
 SQ SEQUENCE 233 AA; 25658 MW; B940325058D4A03 CRC64;  
 -----  
 Query Match 8.0%; Score 76.5; DB 1; Length 233;  
 Best Local Similarity 21.8%; Pred. No. 2.8;  
 Matches 50; Conservative 34; Mismatches 70; Indels 75; Gaps 11;  
 QY 7 ENPFLSHRTQGAQRSSWKLWFLCSIVMLFLCSFWLIFL----OLETAKEPCMAK 63  
 DB 15 EALPRKTAGQGSRR-CWFLSLFSLVAGATTFLCLLHFGVIGQREFFPKDPSL--IS 71

QY 64 PLPSKQMAS---SEPPCVN-----KVSQWKLLEILQNG 94  
 Db 72 PLAQAVERSSPTSDKPVVHVVPANQAEQOLWLNRRANALLANGVELDNLVVPSEGL 131  
 QY 95 YLIGQV-----APNANY---NDVAPFEVRLYKKNKDMIQTLTNKSIQN----- 135  
 Db 132 YLIYSQVLFKQGCPSNHVLLTHTISRIASVYTKVNLLSAI--KSPQRETPEGAEAKP 189  
 QY 136 -----VGGHYELHVGDTID-----LIFNSEHQLVKNNTYWGIIIL 170  
 Db 190 WYEPYILGVGFQLEKGRDLSAEINLPDYLDFAESQV-----YFGIIA 233  
 RESULT 8  
 YFI4\_FOWP1  
 ID YFI4\_FOWP1 STANDARD; PRT; 129 AA.  
 AC P21972;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE HYPOTHETICAL 14.1 KDA PROTEIN.  
 GN FPI4.  
 OS Fowlpox virus (strain FP-1).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Avipoxvirus.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90324937; PubMed=2165135;  
 RA Tartaglia J., Winslow J., Goebel S., Johnson G.P., Taylor J.,  
 RA Paoletti E.;  
 RT "Nucleotide sequence analysis of a 10.5 kbp HindIII fragment of  
 RT fowlpox virus: relatedness to the central portion of the vaccinia  
 RT virus HindIII D region."  
 RL J. Gen. Virol. 71:1517-1524 (1990).  
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 CC -----  
 DR EMBL; X62141; CAA44068.1; -  
 DR PIR; S22052; S22052.  
 DR HSSP; P01375; ITNF.  
 DR INTERPRO; IPR000478; -  
 DR INTERPRO; IPR002959; -  
 DR PFAM; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRINTS; PR01235; TNALPHA.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS0049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;  
 KW Myristate.  
 FT PROPEP 1 76 BY SIMILARITY.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT LIPID 19 19 MYRISTATE (BY SIMILARITY).  
 FT LIPID 20 20 MYRISTATE (BY SIMILARITY).  
 FT DISULFID 145 177 BY SIMILARITY.  
 SQ SEQUENCE 129 AA; 14110 MW; E0C25E79875E40DB CRC64;

Query Match 7.9%; Score 75; DB 1; Length 129;  
 Best Local Similarity 28.8%; Pred. No. 1.9;  
 Matches 23; Conservative 14; Mismatches 37; Indels 6; Gaps 3;  
 QY 31 SIYMLFLCFSWLIIFLQLETAKEPCMAKFGPLPSKWQW---ASSEPPCVNKNVSDWL 87  
 Db 6 SIYVLTWIGSCFYNPFT-LTYECRDCCNGRYGVPAPKVLNCTKTGPGCPD--SGYLL 62  
 QY 88 EILQNGLYLIYGOVAPNANY 107  
 Db 63 TTSENKTYCITGNETDKGY 82

RESULT 9  
 TNFA\_PAPSP  
 ID TNFA\_PAPSP STANDARD; PRT; 233 AA.  
 AC P33620;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
 GN TNF OR TNFA.  
 OS Papio sp. (Baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Papio.  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RA Sanjanwala M., Edwards A.;  
 RL submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.  
 CC FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
 CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
 CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
 CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CC CONDITIONS.  
 CC SUBUNIT: HOMOTRIMER.  
 CC SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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 CC -----  
 DR EMBL; X62141; CAA44068.1; -  
 DR PIR; S22052; S22052.  
 DR HSSP; P01375; ITNF.  
 DR INTERPRO; IPR000478; -  
 DR INTERPRO; IPR002959; -  
 DR PFAM; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRINTS; PR01235; TNALPHA.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS0049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;  
 KW Myristate.  
 FT PROPEP 1 76 BY SIMILARITY.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR.  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT LIPID 19 19 MYRISTATE (BY SIMILARITY).  
 FT LIPID 20 20 MYRISTATE (BY SIMILARITY).  
 FT DISULFID 145 177 BY SIMILARITY.  
 SQ SEQUENCE 233 AA; 25557 MW; 455360B48DC74173 CRC64;

Query Match 7.8%; Score 74.5; DB 1; Length 233;  
 Best Local Similarity 21.2%; Pred. No. 4.3;  
 Matches 51; Conservative 28; Mismatches 63; Indels 99; Gaps 12;  
 QY 7 ENMPLSHSRTOGAQRSSWKLWLFCSIVMLFLCFSFWL-----IFIFLQL----- 51  
 Db 15 EALPKTKGFGQSR-----CLFLSLFSLVAGATFLFCLLHFGVGPQRE 61  
 QY 52 ETAKPEPCMAKFGPLPSKWQMAS---SEPPCVNKNV----- 83  
 Db 62 EFPKDFSL--ISPLAQAVRSSRTPSDKPVAVHVANPQAEQOLWLNRRANALLANGVEL 119  
 QY 84 -DWKLEILQNGLYLIYGOV-----APNANY---NDVAPFEVRLYKKNKDMIQTLTNKSI 133  
 Db 120 RDNQLVVPSEGLYLIYSQVLFKQGCPSHTVLTHTISRIASVYTKVNLLSAI--KSPC 177  
 QY 134 QN-----VGGTYELHVGDTID-----LIFNSEHQLVKNNTYWGIIIL 169  
 Db 178 QRTPECAEAKPWYEPYILGVGFQLEKGRDLSAEINLPDYLDFAESQV-----YFGIIA 232  
 QY 170 L 170  
 Db 233 L 233

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RESULT 10
ID GBI_HOMAM STANDARD; PRT; 354 AA.
AC P41776;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1), ALPHA SUBUNIT (ADENYLATE
DE CYCLASE-INHIBITING G-ALPHA PROTEIN).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OLFACTORY ORGAN;
RX MEDLINE=93061797; PubMed=1279345;
RA McClintock T.S., Byrnes A.P., Lerner M.R.;
RT "Molecular cloning of a G-protein alpha i subunit from the lobster
RT olfactory organ.";
RL Brain Res. Mol. Brain Res. 14:273-276(1992).
CC -!- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
CC INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE
CC SIGNALING SYSTEMS.
CC -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
CC -!- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1
CC (G1/O/T/2).
CC -----
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CC -----
DR EMBL; S47614; CAB29288.1; ALT_SEQ.
DR PIR; A48976; A48976.
DR HSP; P10824; 1A53.
DR INTERPRO; IPR001019; -.
DR INTERPRO; IPR001408; -.
DR PFAM; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR00441; GPROTEINAI.
DR GTP-binding; Transducer; ADP-ribosylation; Multigene family;
KW Myristate.
FT INIT_MET 0 0 BY SIMILARITY.
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT NP_BIND 40 47 GTP (BY SIMILARITY).
FT NP_BIND 200 203 GTP (BY SIMILARITY).
FT NP_BIND 269 272 GTP (BY SIMILARITY).
FT MOD_RES 178 178 ADP-RIBOSYL[1] (BY ACTION OF CTX)
FT MOD_RES 351 351 ADP-RIBOSYL[1] (BY ACTION OF IAP)
FT MOD_RES 351 351 ADP-RIBOSYL[1] (BY SIMILARITY).
FT CONFLICT 308 323 MISSING (IN CAB29288).
FT SEQUENCE 354 AA; 40600 MW; 1A032BCEFF83896D CRC64;

Query Match 7.8%; Score 74.5; DB 1; Length 354;
Best Local Similarity 23.5%; Pred. No. 6.9;
Matches 36; Conservative 30; Mismatches 72; Indels 15; Gaps 6;

QY 18 GAORSSKWLWFC--SIYVLLFLCSFSLWLIFFIQLQETAKE--PCMAKFGPL-PSKWQMA 72
DB 202 GQORSEKKNWICHCEGVTAIIIFVVALSGYDLVLAEDEEMNRMIESMKLFDSICNNKWFVE 261
QY 73 SSEPCVKNVSDWKLEILQNGLYLYIGVAPNANYNDVAPFEVRLYKKNKMIQTLTKSK 132
DB 262 TSIIILFNKDLFEQKITKSPITCFEYQGSNYVEDSANYIRMKFEN-----LNKRK 314

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QY 133 IQNVGGTYELHWGDT--IDLIFNSEHOV-LKNN 162
DB 315 DQKELYTHFTCATDTNNIQFVDFDVTVIKNN 347

RESULT 11
ID TRA3_MOUSE STANDARD; PRT; 567 AA.
AC Q60803; Q62380;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)
DE (CRAF1) (TRAFAMN).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498(1995).
RN [2]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6J; TISSUE=BRAIN;
RX MEDLINE=96299439; PubMed=8660894;
RA Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lonberg N.,
RA Dinullos M.B., Distche C.M., Copeland N., Gilbert D.J., Jenkins N.A.,
RA Lacy E.;
RT "A candidate gene for the amniotless gastrulation stage mouse mutation
RT encodes a TRAF-related protein.";
RL Dev. Biol. 177:274-290(1996).
CC -!- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
CC ASSOCIATED FACTORS (POTENTIAL).
CC -!- TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN
CC KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT
CC FOUND IN LIVER.
CC -!- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST
CC LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION,
CC FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
CC -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC -!- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
CC -----
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CC -----
DR EMBL; U21050; AAC52175.1; -.
DR EMBL; U33840; AAC52710.1; -.
DR MGD; MGI:108041; TRAF3.
DR INTERPRO; IPR001841; -.
DR INTERPRO; IPR002083; -.
DR PFAM; PF00917; MATH; 1.
DR PFAM; PF00097; zf-C3HC4; 1.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
DR Zinc-finger; Coiled coil.
DR ZN_FING 67 76 C3HC4-TYPE.
FT DOMAIN 266 337 COILED COIL (POTENTIAL).
FT DOMAIN 417 502 MATH/TRAF.
FT CONFLICT 72 73 CE -> WQ (IN REF. 2).
FT CONFLICT 390 390 "T -> M (IN REF. 2).
FT SEQUENCE 567 AA; 64263 MW; 2522B343B41192DC CRC64;

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Query Match          7.8%; Score 74; DB 1; Length 567;
Best Local Similarity 28.3%; Pred. No. 13;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 72 ASSEPPCVNKVSDW-----KLEILQNGLYLYIGVAPNAN-----YNDVAFPEVRLYKNK 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 ASSAVQHVNLKWSNLSLEKKVSLQN-----ESVEKNKSQSLHNOICSFIEIERQK 305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 122 DMIQTITNKSKTIONGGTYELHVGDTIDLFNSEHQVLK 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 306 EMLR--NNESKI-----LHLQRLVID-----SQAELK 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
TRA3_HUMAN
ID TRA3_HUMAN STANDARD; PRT; 568 AA.
AC Q13114; Q13076; Q13947; Q12990;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)
DE (CRAF1) (CD40 BINDING PROTEIN) (CD40BP) (LMP1 ASSOCIATED PROTEIN)
DE (LAP1).
DE TRAF3 OR CRAF1 OR CAP-1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC [1]
RN SEQUENCE FROM N.A.
RP MEDLINE-95184010; PubMed-7533327;
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
RL Science 267:1494-1498 (1995).
RN [2]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP TISSUE-LYMPHOMA;
RA Mosialos G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C.,
RT Kieff E.;
RT "The Epstein-Barr virus transforming protein LMP1 engages signaling
RT proteins for the tumor necrosis factor receptor family.";
RL Cell 80:389-399 (1995).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=FETAL BRAIN;
RA Sato T., Irie S., Reed J.C.;
RT "A novel member of the TRAF family of putative signal transducing
RT proteins binds to the cytosolic domain of CD40.";
RL FEBS Lett. 358:113-118 (1995).
RN [4]
RN SEQUENCE FROM N.A.
RP MEDLINE-95073988; PubMed-7527023;
RA Hu H.M., O'Rourke K., Boguski M.S., Dixit V.M.;
RT "A novel ring finger protein interacts with the cytoplasmic domain of
RT CD40.";
RL J. Biol. Chem. 269:30069-30072 (1994).
RN [5]
RN FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
RN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
RN TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.
RN -!- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
RN ASSOCIATED FACTORS (POTENTIAL).
RN -!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
RN -!- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
RN -----
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CC EMBL; U21092; AAC50112.1; -
DR EMBL; U19260; AAA65732.1; -
DR EMBL; L38509; AAA68195.1; -
DR EMBL; U15637; AAA56753.1; -
DR MM; 601896; -
DR INTERPRO; IPR001841; -
DR INTERPRO; IPR002083; -
DR PFAM; PF00917; MATH; 1.
DR PFAM; PF00917; 2f-C3HC4; 1.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
KW Zinc-finger; Coiled coil.
FT ZN_FING 68 77 C3HC4-TYPE.
FT DOMAIN 267 338 COILED COIL (POTENTIAL).
FT DOMAIN 418 503 MATH/TRAF.
FT CONFLICT 129 129 T -> M (IN REF. 2 AND 4).
FT CONFLICT 134 134 MISSING (IN REF. 4).
FT CONFLICT 218 242 MISSING (IN REF. 3).
FT CONFLICT 339 339 P -> S (IN REF. 3).
FT CONFLICT 405 405 R -> G (IN REF. 4).
SQ SEQUENCE 568 AA; 64460 MW; 6765533FBF523C8B CRC64;

Query Match          7.8%; Score 74; DB 1; Length 568;
Best Local Similarity 28.3%; Pred. No. 13;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 72 ASSEPPCVNKVSDW-----KLEILQNGLYLYIGVAPNAN-----YNDVAFPEVRLYKNK 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 253 ASSAVQHVNLKWSNLSLEKKVSLQN-----ESVEKNKSQSLHNOICSFIEIERQK 306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 122 DMIQTITNKSKTIONGGTYELHVGDTIDLFNSEHQVLK 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 307 EMLR--NNESKI-----LHLQRLVID-----SQAELK 331
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
REAL_XENLA
ID RFAI_XENLA STANDARD; PRT; 609 AA.
AC Q01588;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE REPLICATION PROTEIN A 70 KDA DNA-BINDING SUBUNIT (RP-A) (RF-A)
DE (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING
DE PROTEIN).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OC [1]
RN SEQUENCE FROM N.A.
RP TISSUE=OOCYTE;
RX MEDLINE-92407024; PubMed-1527163;
RA Adachi Y., Laemmli U.K.;
RT "Identification of nuclear pre-replication centers poised for DNA
RT synthesis in Xenopus egg extracts: immunolocalization study of
RT replication protein A.";
RL J. Cell Biol. 119:11-15 (1992).
CC -!- FUNCTION: ABSOLUTELY REQUIRED FOR SIMIAN VIRUS 40 DNA REPLICATION
CC IN VITRO. IT PARTICIPATES IN A VERY EARLY STEP IN INITIATION. RP-A
CC IS A SINGLE-STRANDED DNA-BINDING PROTEIN.
CC -!- SUBUNIT: HETERODIMER OF 70, 32, AND 14 KDA CHAINS. THE
CC DNA-BINDING ACTIVITY MAY RESIDE EXCLUSIVELY ON THE 70 KDA SUBUNIT.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: TO OTHER SPECIES RFA2/RPA2.
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DR PIR: S12723; S12723.
DR HSP; P07353; 1RFB.
DR INTERPRO; IPR002069; -.
DR PFAM; PF00714; IFN-gamma; 1.
DR Cytokine; Antiviral; Growth regulation; Immunomodulation;
KW Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 166 INTERFERON GAMMA.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ SEQUENCE 166 AA; 19369 MW; 9232D31269805D0A CRC64;

Query Match 7.7%; Score 73; DB 1; Length 166;
Best Local Similarity 27.7%; Pred. No. 4;
Matches 38; Conservative 22; Mismatches 49; Indels 28; Gaps

QY 22 SSKWLFCISVIMLFLGSPSWLFIPIQLQETAKE-----PCMAKFGPLPSKWMASSE 75
DB 5 SSFLALLLC--VLLGFGSGYCGQGF-PKEIENIKYFNASNPDVAKGGLPSE-----54
QY 76 PPCNVKVSQDKLE-----ILQNGLYLIQGVAPNANTNDVAPEVRLYKKNKDMIOITLTKS 131
DB 55 -----ILKNWKEESKKLIQSOIVSFYFKLFENLKDQVQIORSMDIIR-QDMFQKFLNGS 108
QY 132 --KIONVGQGTVELHVGVD 146
DB 109 SEKLEDFKRLQIPVDD 125

RESULT 15
VS09_ROTHS
ID VS09_ROTHS STANDARD; PRT: 326 AA.
AC P04510;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE GLYCOPROTEIN VP7 (SEROTYPE-SPECIFIC ANTIGEN) (OUTER SHELL
DE GLYCOPROTEIN).
DE S9.
OS Human rotavirus (serotype 2 / strain S2).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
RP 111
RP SEQUENCE FROM N.A.
RX MEDLINE=88044489; PubMed=2823458;
RA Green K.Y., Midhun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,
RA Chanock R.M., Flores J.;
RT "Comparison of the amino acid sequences of the major neutralization
RT protein of four human rotavirus serotypes.";
RL Virology 161:153-159(1987).
RP 121
RP SEQUENCE FROM N.A.
RP Both G.W.;
RA Submitted (MAR-1985) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.
CC -!- SUBCELLULAR LOCATION: ROUGH ENDOPLASMIC RETICULUM.
CC -----
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CC -----
EMBL; M11164; AAA47312.1; -.
DR PIR: H27620; VQXR2S.
DR PIR: A42133; VQXR3S.
DR INTERPRO; IPR001963; -.
DR PFAM; PF00434; VP7; 1.
KW Coat protein; Transmembrane; Glycoprotein.
FT TRANSMEM 32 48 POTENTIAL.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).

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